Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

Claim 1 (currently amended): An assay method, comprising:

(a) providing a plurality of discrete solid support surface areas,

(b) providing a plurality of different ligands,

(c) defining a first set of different groups of the plurality of ligands,

(d) immobilizing each group of ligands on a different solid support surface area,

(e) providing a plurality of different and separate analytes, each of which is capable of binding to a respective one of the plurality of ligands, at least about 75% of the analytes having substantially no cross-reactivity to other ligands,

(f) defining a first set of different groups of the plurality of analytes, each analyte being present in at least one group,

(g) sequentially contacting each group of analytes with the surface areas to bind the analytes in each group to immobilized ligands, and

(h) detecting an interaction of each group of analytes with each group of ligands to determine therefrom an amount of binding of each analyte; and

wherein each of said analytes is not an epitope of a macromolecule having groups of epitopes thereon.

Claim 2 (previously presented): The method according to claim 1, wherein at least about 87.5% of the analytes have substantially no cross-reactivity to other ligands.

Claim 3 (previously presented): The method according to claim 1, wherein at least about 90% of the analytes have substantially no cross-reactivity to other ligands.

Claim 4 (original): The method according to claim 1, wherein none of the different groups of ligands includes all the different ligands.

Claim 5 (original): The method according to claim 1, wherein none of the different groups of analytes includes all the different analytes.

Claim 6 (original): The method according to claim 1, wherein each ligand is present in at least two different groups of ligands.

Claim 7 (original): The method according to claim 1, wherein the groups of ligands and the groups of analytes are defined such that in each group of analytes, each analyte binds specifically to a different one of the different groups of ligands.

Claim 8 (previously presented): The method according to claim 1, wherein steps e) to h) in claim 1 are repeated with a second set of different groups of analytes, differently

defined than the first set, to determine possible influence of other analytes on the binding of a specific analyte to a specific ligand.

Claim 9 (previously presented): The method according to claim 1, wherein steps b) to h) in claim 1 are repeated with a second set of different groups of ligands, differently defined than the first set, to determine possible influence of other ligands on the binding of a specific analyte to a specific ligand.

Claim 10 (original): The method according to claim 1, wherein each group of analytes contains at least three different analytes.

Claim 11 (original): The method according to claim 1, wherein each group of ligands contains at least three different ligands.

Claim 12 (original): The method according to claim 7, which comprises providing a plurality of soluble ligands or ligand analogues which bind specifically to respective ones of the analytes, defining different groups of the soluble ligands or ligand analogues such that one ligand or ligand analogue in each group thereof binds specifically to one analyte in each group of analytes, and prior to step g) in claim 1 mixing each group of ligands or ligand analogues with its respective group of analytes.

Claim 13 (original): The method according to claim 7, wherein prior to step g) in claim 1, each group of analytes is mixed with binding agents that compete with the analytes for the binding to their respective immobilized ligands.

Claim 14 (original): The method according to claim 7, wherein prior to step g) in claim 1, respective specific binding partners to the immobilized ligands are contacted with the different solid support surface areas.

Claim 15 (previously presented): The method according to claim 1, wherein after determining the binding of the analytes in a group in step h) in claim 1, the surface areas are contacted with a regeneration solution, and capability of the regeneration solution to remove each analyte from its ligand is determined.

Claim 16 (original): The method according to claim 15, wherein the surface areas subjected to regeneration solution are sequentially contacted with the different groups of analytes to determine any change in binding in relation to that determined in step h) in claim 1.

Claim 17 (original): The method according to claim 15, which is repeated with at least one different regeneration solution.

Claim 18 (original): The method according to claim 1, wherein the solid support areas are sensing surface areas.

Claim 19 (original): The method according to claim 1, wherein the interactions at the surface are monitored in real time.

Claim 20 (original): The method according to claim 1, wherein mass changes at the surface areas are detected.

Claim 21 (previously presented): The method according to claim 1, wherein the detection is evanescent wave sensing.

Claim 22 (previously presented): The method according to claim 1, wherein the detection is surface plasmon resonance (SPR).

Claim 23 (original): The method according to claim 18, wherein the sensing surface areas are provided in at least one flow cell.

Claim 24 (original): The method according to claim 1, which comprises determining at least one of ligand immobilization efficiency, analyte concentration, interaction affinity and interaction kinetics.

Claims 25-32 (cancelled)

Claim 33 (currently amended): An assay method comprising:

(a) providing a plurality of discrete solid support surface areas,

(b) providing a plurality of n different ligands, wherein n is at least 2,

(c) defining different groups of the plurality of n ligands comprising single ligands and combinations of from two to n different ligands,

(d) immobilizing each group of ligands on a different surface area,

(e) sequentially contacting a plurality of n different and separate analytes with each surface area, at least about 75% of the analytes being capable of specifically binding to a respective one of the plurality of different ligands, and

(f) detecting an interaction of each analyte with each group of ligands to determine therefrom an amount of ligand-binding of each analyte, and possible influence of ligand-ligand interaction on the binding of analyte to immobilized ligand; and

wherein each of said analytes is not an epitope of a macromolecule having groups of epitopes thereon.

Claim 34 (previously presented): The method according to claim 33, wherein at least about 87.5% of the analytes are capable of specifically binding to a respective one of the plurality of ligands.

Claim 35 (previously presented): The method according to claim 33, wherein at least about 90% of the analytes are capable of specifically binding to a respective one of the plurality of ligands.

Claim 36 (original): The method according to claim 33, wherein in step e) in claim 33, the surface areas are sequentially contacted with different groups of analytes, comprising single analytes and combinations of from two to n different analytes.

Claim 37 (previously presented): The method according to claim 33, wherein the solid support areas are sensing surface areas, and the detection is evanescent wave sensing.

Claim 38 (original): The method according to claim 33, which comprises determining at least one of ligand immobilization efficiency, analyte concentration, interaction affinity and interaction kinetics.

Claims 39-47 (cancelled)

Claim 48 (currently amended): An assay method comprising:

(a) providing a plurality of discrete solid support surface areas,

(b) providing a plurality of different ligands,

(c) defining different groups of the plurality of ligands,

(d) immobilizing each group of ligands on a different solid support surface area,

(e) providing a plurality of different and separate analytes, each of which is capable of binding to a respective one of the plurality of ligands, at least about 75% of the analytes having substantially no cross-reactivity to other ligands,

(f) sequentially contacting each analyte with the surface areas to bind the analytes to the immobilized ligands, and

(g) detecting an interaction of analyte with each group of immobilized ligands to determine therefrom an amount of binding of each analyte; and

wherein each of said analytes is not an epitope of a macromolecule having groups of epitopes thereon.

Claim 49 (previously presented): The method according to claim 48, wherein at least about 87.5% of the analytes have substantially no cross-reactivity to other ligands.

Claim 50 (previously presented): The method according to claim 48, wherein at least about 90% of the analytes have substantially no cross-reactivity to other ligands.

Claim 51 (previously presented): The method according to claim 48, wherein the solid support areas are sensing surface areas, and the detection is evanescent wave sensing.

Claim 52 (original): The method according to claim 48, which comprises determining at least one of ligand immobilization efficiency, analyte concentration, interaction affinity and interaction kinetics.

Claims 53-64 (cancelled)